1 LARA

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DATE: 11/06/2000

TIME: 11:22:56

HECENE Bage 1 of 7

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/348,815

Input Set : A:\126pld1-sl.txt

Output Set: N:\CRF3\11062000\I348815.raw

## SEQUENCE LISTING

```
(1) GENERAL INFORMATION:
             (i) APPLICANT: LI, HAODONG
                            ADAMS, MARK D
     9
            (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR-2
           (iii) NUMBER OF SEQUENCES: 6
     1.1
            (iv) CORRESPONDENCE ADDRESS:
     1.3
                  (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
     14
                  (B) STREET: 9410 KEY WEST AVENUE
     1.5
     1.6
                  (C) CITY: ROCKVILLE
                  (D) STATE: MD
     17
                  (E) COUNTRY: US
     18
     19
                  (F) ZIP: 20850
     21.
             (V) COMPUTER READABLE FORM:
                  (A) MEDIUM TYPE: Floppy disk
     22
     23
                  (B) COMPUTER: IBM PC compatible
     24
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     25
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
            (vi) CURRENT APPLICATION DATA:
     27
C--> 28
                  (A) APPLICATION NUMBER: US/09/348,815
C-->
    29
                  (B) FILING DATE: 08-Jul-1999
     30
                  (C) CLASSIFICATION:
     32
          (viii) ATTORNEY/AGENT INFORMATION:
     33
                  (A) NAME: JONATHAN L. KLEIN
                  (B) REGISTRATION NUMBER: 41,119
     34
     35
                  (C) REFERENCE/DOCKET NUMBER: PF126P1D1
     37
            (ix) TELECOMMUNICATION INFORMATION:
     38
                  (A) TELEPHONE: 301-309-8504
     39
                  (B) TELEFAX: 301-309-8439
     42 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     4.4
     45
                  (A) LENGTH: 1146 base pairs
                  (B) TYPE: nucleic acid
     47
                  (C) STRANDEDNESS: single
                 · (D) TOPOLOGY: linear
     48
     50
            (ii) MOLECULE TYPE: DNA (genomic)
     53
            (ix) FEATURE:
     54
                  (A) NAME/KEY: CDS
                  (B) LOCATION: 1..1146
     55
     58
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
     60 ATG AGC TCC CGC ATC GCC AGG GCG CTC GCC TTA GTC GTC ACC CTT CTC
     61 Met Ser Ser Arg lle Ala Arg Ala Leu Ala Leu Val Val Thr Leu Leu
                          5
                                              1.0
     64 CAC THG ACC AGG CTG GCG CTC TCC ACC TGC CCC GCT GCC TGC CAC TGC
                                                                            96
     65 His Leu Thr Arg Leu Ala Leu Ser Thr Cys Pro Ala Ala Cys His Cys
                     20
                                          25
```

68 CCC CTG GAG GCG CCC AAG TGC GCG CCG GGA GTC GGG CTG GTC CGG GAC

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/348,815 DATE: 11/06/2000 TIME: 11:22:56

Input Set : A:\126pldl-s1.txt
Output Set: N:\CRF3\11062000\1348815.raw

Pro	Leu	Glu 35	Ala	Pro	Lys	Суѕ	Ala 40	Pro	Gly	Val	Gly	Leu 45	Val	Arg	Asp	
GGC	TGC		TGC	TIGT	AAG	GTC		GCC	AAG	CAG	CTC		GAG	GAC	TGC	192
•	50	••	•	1		55					60				- , -	
AGC	AAA	ACG	CAG	CCC	TGC	GAC	CAC	ACC	AAG	GGG	CTG	GAA	TGC	AAC	TTC	240
ser	Lys	Thr	Gln	Pro	Cys	Asp	Hi.s	Thr	Lys	Gly	Leu	G ].u	Суѕ	Asn	Phe	
65					70					75					8.0	
																288
Gly	Ala	Ser	Ser		Ala	Leu	Lys	Gly		Cys	Arg	Ala	Gln		Glu	
																336
G.I.Y	Arg	Pro	-	GIU	туг	ASN	Ser		1.i.e	туr	GIn	ASII	_	GLU	ser	
mme	CAC	ccc		חיכיםי	A A A	Cam	CAC		אריא	mem.	א מימי	۲۰ ۸ (B		ccc	c mc	384
																304
inc	0,411		ДЭП	Cy 3	шуз	1123		Cys	LILL	Cys			G.L y	A1.u	va.L	
GGC	TGC		CCT	CTG	TGT	CCC		GAA	CTA	TCT			AAC	TTG	GGC	432
•	130				_						140					
TGT	CCC	AAC	CCT	CGG	CTG	GTC	AAA	GTT	ACC	GGG	CAG	TGC	TGC	GAG	GAG	480
Cys	Pro	Asn	Pro	Arg	Leu	Va l	Lys	Val.	Thr	G.l y	Gln	Cys	Cys	Glu	G.l.u	
145					150					155					160	
TGG	GTC	TGT	GAC	GAG	GAT	AGT	ATO	AAG	GAC	ccc	ATG	GAG	GAC	CAG	GAC	528
. Trp	Va l	. Cys	Asp	Glu	Asp	Ser	11.e	Lys	Asp	Pro	Met	Glu	Asp	Gln	Λsp	
				165												
																576
	Let	i T.eu	C: 1 sz	1.57 G	Glu	Leu	⊢G,ly			. ∧la		C17				
				11 .5					_	, FLLU	ser	G.1. (J			. Leu	
			180					1.85					1.90	ı		
ACG	AGA	AAC	180 AAT	GAA	TTG			185 GTT	GGA	AAA	. GGC	AGC	190 TCA	CTG	AAG	624
ACG Thr	AGA	AAC Asn	180 AAT Asn	GAA	TTG		Ala	185 GTT Val	GGA	AAA	. GGC	AGC Ser	190 TCA Ser	CTG	AAG	624
ACG Thr	AGA Arç	AAC Asn 195	180 AAT Asn	GAA Glu	TTG Leu	Tle	A.la 200	185 GTT Val	GGA Gly	AAA Lys	GIY GGC	AGC Ser 205	190 TCA Ser	CTG Leu	AAG Lys	
ACG Thr CGG	AGA Arg	AAC Asn 195 CCT	180 AAT Asn	GAA Glu TTT	TTG Leu GGA	Tle	Ala 200 GAG	185 GTT Val	GGA Gly CGC	AAA Lys	GGC GLy	AGC Ser 205	190 TCA Ser	CTG	AAG Lys	624 672
ACG Thr CGG Arg	AGA Arg CTC	AAC Asn 195 CCT Pro	180 AAT Asn	GAA Glu TTT	TTG Leu GGA	Tle ATG Met	Ala 200 GAG	185 GTT Val	GGA Gly CGC	AAA Lys	GGC GLy CTA	AGC Ser 205	190 TCA Ser	CTG	AAG Lys	
ACG Thr CGG Arg	AGA Arg CTC Leu 210	AAC Asn 195 CCT Pro	180 AAT Asn GTT Val	GAA Glu TTT Phe	TTG Leu GGA Gly	ATG Met 215	Ala 200 GAG Glu	185 GTT Val CCT Pro	GGA Gly CGC Arg	AAA Lys ATC	GGC Gly CTA Leu 220	AGC Ser 205 TAC Tyr	190 TCA Ser AAC	CTG Leu CCT Pro	AAG Lys TTA Leu	672
ACG Thr CGG Arg	AGA Arg CTC Leu 210	AAC Asn 195 CCT Pro	180 AAT Asn GTT Val	GAA Glu TTT Phe TGT	TTG Leu GGA Gly	ATG Met 215	Ala 200 GAG Glu	185 GTT Val CCT Pro	GGA Gly CGC Arg	AAAA Lys ATC	GGC Gly CTA Leu 220	AGC Ser 205 TAC Tyr	190 TCA Ser AAC ASn	CTG Leu CCT Pro	AAG Lys TTA Leu	
ACG Thr CGG Arg	AGA Arg CTC Leu 210	AAC Asn 195 CCT Pro	180 AAT Asn GTT Val	GAA Glu TTT Phe TGT	TTG Leu GGA Gly	ATG Met 215 GTT Val	Ala 200 GAG Glu	185 GTT Val CCT Pro	GGA Gly CGC Arg	AAAA Lys ATC	GGC Gly CTA Leu 220 TGG	AGC Ser 205 TAC Tyr	190 TCA Ser AAC ASn	CTG Leu CCT Pro	AAG Lys TTA Leu	672
ACG Thr CGG Arg CAA Gln 3 225	AGA Arg CTC Leu 210	AAC Asn 195 CCT Pro	180 AAT Asn GTT Val AAA Lys	GAA Glu TTT Phe TGT Cys	TTG Leu GGA Gly ATT Ile 230	ATG Met 215 GTT Val	Ala 200 GAG Glu CAA Gln	185 GTT Val CCT Pro	GGA Gly CGC Arg ACT	A AAAA Lys ATC	GGC Gly CTA Leu 220 TGG	AGC Sen 205 TAC Tyr TCC Sen	190 TCA Ser AAC Asn CAG	CTG Leu CCT Pro TGC Cys	AAG Lys TTA Leu TCA Ser 240	672
ACG Thr CGG Arg CAA CAA CAA CAA	AGA CTC Leu 210 GGC Gly	A AAC Asn 195 CCT Pro	180 AAT Asn GTT Val AAA Lys	GAA Glu TTT Phe TGT Cys	TTG Leu GGA Gly ATT Ile 230 GGT	ATG Met 215 GTT Val	Ala 200 GAG Glu CAA Gln	185 GTT Val CCT Pro ACA Thr	GGA Gly CGC Arg ACT Thr	A AAAA Lys ATC ATC Ile TCA Ser 235	GGC GLy CTA Leu 220 TGG Trp	AGC Ser 205 TAC Tyr TCC Ser	190 TCA Ser AAC Asn CAG	CTG Leu CCT CCT CCT CCT CCT CCT CCT CCT CCT CC	AAG Lys TTA Leu TCA Ser 240	672 720
ACG Thr CGG Arg CAA CAA CAA CAA	AGA CTC Leu 210 GGC Gly	A AAC ASN 195 CCT Pro CAG Gln	180 AAT Asn GTT Val AAA Lys	GAA Glu TTT Phe TGT Cys	TTG Leu GGA Gly ATT Ile 230 GGT	ATG Met 215 GTT Val	Ala 200 GAG Glu CAA Gln	185 GTT Val CCT Pro ACA Thr	GGA Gly CGC Arg ACT Thr	A AAAA Lys ATC ATC TCA Ser 235	GGC GLy CTA Leu 220 TGG Trp	AGC Ser 205 TAC Tyr TCC Ser	190 TCA Ser AAC Asn CAG	CTG Leu CCT CCT CCT CCT CCT CCT CCT CCT CCT CC	AAG Lys TTA Leu TCA Ser 240 CCT Pro	672 720
ACG Thr CGG Arg CGAA CAA CAA CAA CAA CAA CAA CAA CAA CA	AGA CTC Leu 210 GGC Gly ACC	A AAC ASN 195 CCT Pro CAG Gln	AAA Lys	GAA Glu TTT Phe TGT Cys ACT Th.c 245	TTG Leu GGA Gly ATT Ile 230 GGT Gly	ATG Met 215 GTT Val ATG	Ala 200 GAG Glu CAA Gln	185 GTT Val CCT Pro ACA Thr	GGA Gly CGC Arg ACT Thr CGA Arg 250	A AAA  Lys  ATC  Ile  TCA  Ser  235  GTT  Val	GGC GLy CTA Leu 220 TGG Trp	AGC Ser 205 TAC Tyr TCC Ser AAT	190 TCA Ser AAC Asn CAG Gln	CTG Leu CCT CCT CCT CCT CCT CCT CCT AAC ASn 255	TCA Ser 240 CCT Pro	672 720
B ACG Thr C CGG Arg C CAA C Gln B 225 AAG Lys C GAG	ACC Thr	A AAC Asn 195 C CCT Pro C CAG Gln C TGT	AAA Lys GGA Gly	GAA Glu TTT Phe TGT Cys ACT Th.c 245 GTG	TTG Leu GGA Gly ATT Ile 230 GGT Gly	ATG Met 215 GTT Val ATG Ile	Ala 2000 GAG Glu CAA Gln TCC Ser	185 GTT Val CCT Pro ACA Thr CGG	GGA Gly CGC Arg ACT Thr CGA Arg 250 ATT	A AAA  Lys  ATC  TCA  TCA  Sen  235  GTT  Val	GGC GLy CTA Leu 220 TGG Trp ACC Thr	AGC Ser 205 TAC Tyr TCC Ser AAT Asn	1900 TCAS CAG Glin GAC Asp	CTG Leu CCT Pro TGC Cys AAC Asn 255	TCA Ser 240 CCT Pro	672 720 768
ACGO Thro	ACC Thr	A AAC Asn 195 CCT Pro CAG Gln CTGT Cys CGC Arg	180 AAT Asn GTT Val AAA Lys GGA Gly CTT Leu 260	GAA Glu TTT Phe TGT Cys ACT Thr 245 GTG Val	TTG Leu GGA Gly ATT Ile 230 GGT Gly AAA Lys	ATG Mett 215 GTT Val ATC Ile GAA Glu	Ala 200 GAG Glu CAA Gln TCC Ser	185 GTT Val CCT Pro ACA Thr ACA Thr CGG Arg 265	GGA Gly CGC Arg ACT Thr CGA Arg 250 ATT	A AAA  Lys  TCA  TCA  Ser  235  GTT  Val  TGT  Cys	GGC GTY CTA Leu 220 TGG Trp ACC Thr	AGC Ser 205 TAC Tyr TCC Ser AAT Asn GTG Val	1900 TCAS Ser AAC CAG Gln Asp CGG Arg 270	CTG Leu CCT Pro TGC Cys AAC Asn 255 CCT	AAG Lys TTA Leu TCA Ser 240 CCT Pro	672 720 768 816
ACG Thr CCAA CCAA CCAA CCAA CCAA CCAA CCAA CC	AGA CTC Leu 210 GGC Gly ACC Thr	A AAC Asn 195 CCT Pro CAG Gln CTGT Cys CGC Arg	AAA Lys GGA GLy CTT Leu 260 GTG	GAA Glu TTT Phe TGT Cys ACT Thr 245 GTG Val	TTG Leu GGA Gly ATT Ile 230 GGT Gly AAA Lys	ATG Met 215 GTT Val ATG Ile GAA Glu	Ala 200 GAG GIU CAA GIN ACC Thr	185 GTT Val CCT Pro ACA Thr CGG Arg 265 AAA	GGA Gly CGC Arg ACT Thr CGA Arg 250 ATT Ile	A AAAA Lys ATC Ile Ser 235 GTT Val	GGC Gly CTA Leu 220 TGG Trp ACC Thr	AGC Ser 205 TAC Tyr TCC Ser AAT Asn GTG Val	1900 TCAS Ser AAC AS AS GIN AS CAG AT GAC AT	CTG CCT Pro TGC Cys AAC Asn 255 CCT Pro	AAG Lys TTA Leu TCA Ser 240 CCT Pro TGT Cys	672 720 768
ACGO Thro	AGA CTC Leu 210 GGC Gly ACC Thr	A AAC ASS ASS ASS CCT Pro CAG CAG CYS	AAA Lys GGA Gly CTT Leu 260 GTG Val	GAA Glu TTT Phe TGT Cys ACT Thr 245 GTG Val	TTG Leu GGA Gly ATT Ile 230 GGT Gly AAA Lys	ATG Met 215 GTT Val ATG Ile GAA Glu	Ala 2000 GAG GIU CAA GIN TCC Ser Thr	185 GTT Val CCT Pro ACA Thr CGG Arg 265 AAA Lys	GGA Gly CGC Arg ACT Thr CGA Arg 250 ATT Ile	A AAAA Lys ATC Ile Ser 235 GTT Val	GGC Gly CTA Leu 220 TGG Trp ACC Thr	AGC Ser 205 TAC TYr TCC Ser AAT ASD Val	1900 TCAS Series AACC Asn Gln Asp CGG Arg 270 Cys	CTG CCT Pro TGC Cys AAC Asn 255 CCT Pro	AAG Lys TTA Leu TCA Ser 240 CCT Pro TGT Cys	672 720 768 816
ACGO Thro	AGA Arg CTC Leu 210 GGC Gly ACC Thr Cys	A AAC Asn 195 CCT Pro CAG CAG CYS CGC Arg CCA Pro 275	AAA Lys GGA GLY CTT Leu 260 GTG Val	GAA Glu TTT Phe TGT Cys ACT Thr 245 GTG Val	TTG Leu GGA Gly ATT Ile 230 GGT Gly AAA Lys	ATC Met 215 GTT Val ATC Ile GAA Glu AGC Ser	Alaa 2000 GAG GIU CAA GIN TCC TCC Thr	185 GTT Val CCT Pro ACA Thr CGG Arg 265 AAA Lys	GGAArg ACT Thr CGA Arg 250 ATT Ile	A AAA  Lys  TCA  TCA  Ser  235  GTT  TGT  CYS  GGC  GLY	GGC GLY CTA Leu 220 TGG Trp ACC Thr GAG Glu AAG Lys	AGC Ser 205 TACC Ser AAT Asn GTG Val AAA Lys 285	1900 Service Associated Associate	CTG Leu CCT Pro TGC Cys AAC ASS 255 CCT Pro	AAG Lys TTA Leu TCA Ser 240 CCT Pro TGT Cys AAG	672 720 768 816 864
ACGO Thr. COMMAND COMM	AGA ACC CTC Lett 210 GGy ACC Thr CCys CAG Gln AAG	A AAC ASS ASS ASS CCT Pro CAG CAG CYS	AAAA Lys GGAGA GLY CTT Leu 260 GTG Val	GAA Glu TTT Phe TGT Cys ACT Thr 245 GVal TAC Tyr	TTG Leu GGA Gly ATT Ile 230 GGT Gly AAA Lys AGC Ser	ATG Met 215 GTT Val ATC Ile GAA Glu AGC Ser	Ala 200 GAG Glu CAA Gln CTG Ser CTG Leu 280 GTC	185 GTT Val CCT Pro ACA Thr ACA Thr CGG 265 AAA Lys	GGAArg ACT Thr CGA Arg 250 ATT Ile AAG Lys	AAAA  Lys  ATC  Ile  TCA  Ser  235  GTT  Val  TGT  GGC  GGC  GGC  ACT  ACT  AAAA  AAAA  ACT  AAAA  AAAA  AAAA  AAAA  AAAA  AAAA  AAAA	GGC GLy CTA Leu 220 TGG Trp ACC Thr GAG Glu AAG Lys	AGC Ser 205 TAC Ser AAT ASD GTG Val AAA Lys 285 GCT	1900 TCA Ser AACO ASP GAC ASP CGG ATG CCys	CTGC Leu CCTG Pro CTGC Cys AAC ASn 255 CCT Pro AGC Ser	AAG Lys TTA Leu TCA ser 240 CCT Pro TGT Cys AAG Lys	672 720 768 816
	GLy  AGC GC GLY  TTC Phe GGC GLY  TGT CYS 145 ) TGG	Gly Cys 50 AGC AAA Ser Lys 65 GGC GCC Gly Ala GGC AGA Gly Arg TTC CAG Phe Gln GGC TGC Gly Cys 130 TGT CCC Cys Pro 145 TGG GTC TTP Val	Gly Cys Gly 50  AGC AAA ACG Ser Lys Thr 65  GGC GCC AGC Gly Ala Ser  GGC AGA CCC Gly Arg Pro  TTC CAG CCC Phe Gln Pro 115 GGC TGC ATT Gly Cys Ile 130  TGT CCC AAC Cys Pro Asn 145 ) TGG GTC TGT TTP Val Cys	Gly Cys Gly Cys 50  AGC AAA ACG CAG Ser Lys Thr Gln 65  GGC GCC AGC TCC Gly Ala Ser Ser  GGC AGA CCC TGT Gly Arg Pro Cys 100 TTC CAG CCC AAC Phe Gln Pro Asn 115  GGC TGC ATT CCT Gly Cys Ile Pro 130  TGT CCC AAC CCT Cys Pro Asn Pro 145 0 TGG GTC TGT GAC TTP Val Cys Asp	Gly Cys Gly Cys Cys	Gly Cys Gly Cys Cys Lys	Gly	Gly	Gly Cys Gly Cys Cys Lys Val. Cys Ala 50  AGC AAA ACG CAG CCC TGC GAC CAC ACC Ser Lys Thr Gln Pro Cys Asp His Thr 65 70  GGC GCC AGC TCC ACC GCT CTG AAG GGG Gly Ala Ser Ser Thr Ala Leu Lys Gly 85  GGC AGA CCC TGT GAA TAT AAC TCC AGA CAC ACG ACG ACG ACG ACG ACG ACG A	GIY CYS GIY CYS CYS LYS VAI CYS Ala LYS 50	GIY CYS GIY CYS CYS LYS VAI CYS Ala LYS GIN	GIY CYS GIY CYS CYS LYS VAI CYS Ala LYS GIN LEU	GIY   Cys   GIY   Cys   Cys   Cys   Cys   Tys   Val   Cys   Ala   Lys   GIn   Len   Asn   55   60	GIY CYS GIY CYS CYS CYS LYS VAI CYS Ala LYS GIN Len ASN GIU	Gly Cys Gly Cys Cys Cys Lys Val Cys Ala Lys Gln Leu Asn Glu Asp	AGC AAA ACG CAG CCC TGC GAC CAC ACC ACC ACG CTG GAA TGC AAC TTC ACG CGC GCC ACG ACG ACG ACG ACG CTG GAA ACC ACC ACG ACG ACG ACC ACG ACG AC

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/348,815 DATE: 11/06/2000 TIME: 11:22:56

Input Set : A:\126pld1-s1.txt
Output Set: N:\CRF3\11062000\1348815.raw

134		290					295					300					
1.36	AGT	GTG	AAG	AAA	TAC	CGG		AAG	TAC	TCC	GGT		TGC	GTG	GAC	GGC	960
					Tyr												
	305		•		•	310		•	1		315					320	
140	CGA	TGC	TGC	ACG	CCC	CAG	CTG	ACC	AGG	АСТ	GTG	AAG	ATG	CGG	TTC	CGC	1008
					Pro												
142	•	-	-		325				••	330		* '		,	335		
1.44	TGC	GAA	GAT	GGG	GAG	ACA	TTT	TCC	AAG	λAC	GTC	ATG	ATG	ATC	CAG	TCC	1056
					G l.u												
146				340					345					350			
148	TGC	AAA	TGC	AAC	TAC	AAC	TGC	CCG	CAT	GCC	AAT	GAA	GCA	GCG	TTT	CCC	1104
149	Cys	Lys	Cys	Asn	Tyr	Asn	Cys	Pro	His	Ala	Asn	G1.u	Ala	Ala	Phe	Pro	
150	•	•	355		-		-	360					365				
1.52	TTC	TAC	AGG	CTG	TTC	AAT	GAC	ATT	CAC	AAA	TTT	AGG	GAC	TAA			3.146
					Phe												
154		370					375			-	-	380	•				
157	(2)	INF	ORMA!	PION	FOR	SEQ	ID I	NO: 2	2:								
159		(i	) SE	QUEN	CE CE	HARAG	CTER:	ISTI	CS:								
1.60			(2	A) Li	ENGTI	: 38	31. ar	nino	acio	is							
161			(1	3) T	YPE:	amin	no a	cid									
162			(1	) T(	OLOGIC	OGY:	line	ear									
1.64		( i.i.	) MOI	LECUI	LE TY	YPE:	pro	tein									
1.66		(x.i.	) SE	QUEN	CE DE	ESCR:	rrri	ON: S	SEQ 1	ED NO	): 2	:					
1.68	Met	ser	Ser	Arg	Ile	Ala	Arg	Al.a	Leu	Ala	Leu	Val.	Val	Thr	Leu	Leu	
1.69	1				5					1.0					15		
1.70	His	Leu	Thr	A.r.g	Leu	Ala	Leu	Ser	Thr	Cys	Pro	Ala	A.l.a	Cys	$_{ m H.i.s}$	Cys	
1.71				20					25					30			
	Pro	Leu	Glu	Ala	Pro	Lys	Cys	A.l a	Pro	G.l y	Val	Gly	Leu	Val	Arg	Asp	
1.73			35					40					45				
	Gly	-	Gly	Cys	Cys	_		Cys	Ala	Lys	Gln	Leu	Asn	Glu	Asp	Cys	
1.75		50					. 55					60					
		Lys	Thr	G l.n	Pro		Asp	His	Thr	Lys		Leu	Glu	Cys	Asn	Phe	
177	65					70					75					80	
	GIŸ	Ala	ser	Ser	Thr	Ala	Leu	Lys	G.l. y		Cys	Arg	Ala	Gln		Glu	
179					85					90					95		
	G.I y	Arg	Pro	-	Glu	туг	Asn	Ser	•	Ile	Туr	Gln	Asn	-	Glu	Ser	
1.81		1	_	100	_	_			105					110		_	
	Pne	GIn		Asn	Cys	Lys	His		Cys	Thr	Cys	He	_	GTA	Ala	Val	
183			115		_			120		_		_	125	_			
	GTA	_	1.1G	Pro	Leu	Cys		GIn	GLu	Leu	Ser		P.ro	Asn	Leu	GLY	
1.85	_	130	_	_		_	135	_			79	140	_	_			
	-	P.ro	Asn	Pro	Arg		Val	Lys	Val	Thr	-	GIn	Cys	Cys	GLu		
187		1			49.71	150	a				155		5. 3			160	
	rrp	val	Cys	Asp	Glu	Asp	ser	TTE	Lys		Pro	Met.	G.L.u	Asp		Asp	
1.89	<b>a</b> 3.	<b>.</b>	<b>.</b>	a l	165	a.		cr. T	6.1	170	- 1				1.75		
	G.I.Y	neu	Leu	_	Lys	G.I.U	теп	GTÄ		Asp	A1.a	ser	GLU		G.Lu	Leu	
191	mls -	A	100	180	C1	r	т1-	7 T ~	185	C1	т	C1	0	190	Т « · ·	T	
	THE	wrd		ASII	Glu	теп	т.г.е		Val.i.	U.I.Y	газ	U.I.Y		ser	rien	ьys	
193			195					200					205				

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/348,815 DATE: 11/06/2000 TIME: 11:22:56

Input Set : A:\126pld1-s1.txt
Output Set: N:\CRF3\11062000\1348815.raw

194 195	Arg	Leu 210	Pro	Val	Phe	Gly	Met 215	Glu	P.ro	Arg	Ile	Leu 220	туг	Asn	Pro	Leu	
	Gln		G1.n	Lys	Cys	He		Gln	Thr	Thr	se.r		ser	G.l.n	Cys	Ser	
	225					230					235					240	
198 199	Lys	Thr	Cys	Gly	Thr 245	Gly	Tle	Ser	Thr	Arg 250	Val	Thr	Asn	Asp	Asn 255	Pro	
200 201	Glu	Cys	Arg	Leu 260	Val	Lys	Glu	Thr	Arg 265	Tle	Cys	Gl.u	Val.	Arg 270	Pro	Cys	
	Gly	Gln	Pro 275	Val.	Tyr	ser	ser	Leu 280		Lys	Gly	Lys	Lys 285		ser	Lys	
	Thr	Lys 290		ser	Pro	Glu	Pro 295		Arg	Phe	Thr	Tyr 300		Gly	Cys	Leu	
	Ser		LVS	Lvs	Ψvr	Δεσ		T.ve	Tyr	Cve	Glv		Cue	Val	Aen	Clv	
	305	V C. 1.	цур	пу.5	.t ,y 1.	310	1.10	473	1 y 1.	Cys	315	361	Cys	Val	пэр	320	
	Arg	Cvs	Cvs	Thr	Pro		Leu	Thr	Ara	Thr		Lvs	Met	Ara	Phe		
209	,	•	-		325					330		-2 -		5	335	5	
210	Cys	Glu	Asp	Gly	Glu	Thr	Phe	ser	Lys	Asn	Val	Met	Met	Ile	Gln	Ser	
211				340					345					350			
212	Cys	Lys	Cys	Asn	$\mathbf{T}\mathbf{y}\mathbf{x}$	Asn	Cys	P.ro	His	Ala	Asn	$_{\rm G1u}$	A l.a	Ala	Phe	Pro	
213			355					360					365				
	Phe	-	Arg	Leu	Phe	Asn		Lle	H.i.s	Lys	Phe	-	Asp				
215		370					375					380					
	(2)																
221 222		(1)						ISTIC									
223				•				se pa acio									
224			•					sind									
225				•		OGY:		-	1.1.6								
227		(ii)						(ger	omic	2)							
230								ON: S			): 3:						
232	CGCC																28
234	(2)	INFO	DRMA?	NOL	FOR	SEQ	TD t	10: 4	l :								
236		(i)	SEC	QUENC	CE CE	IARAC	TER	STIC	CS:								
237			( A	4) LE	ENGTI	1: 30	) bas	se pa	irs								
238			(E	3) TY	PE:	nucl	.eic	aci.o	3								
239			((	:) S1	PRANE	DEDNE	ESS:	sing	J.l.e								
240						OGY:											
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DATE: 11/06/2000 TIME: 11:22:56

58

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/348,815

Input Set : A:\126p1d1-s1.txt
Output Set: N:\CRF3\11062000\1348815.raw

264	(2) INFORMATION FOR SEQ ID NO: 6:
266	(i) SEQUENCE CHARACTERISTICS:
267	(Λ) LENGTH: 58 base pairs
268	(B) TYPE: nucleic acid
269	(C) STRANDEDNESS: single
270	· (D) TOPOLOGY: linear
272	(ii) MOLECULE TYPE: DNA (genomic)
275	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
277	CGCTCTAGAT TAAGCGTAGT CTGGGACGTC GTATGGGTAT TGGAACAGCC TGTAGAAG

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/348,815

DATE: 11/06/2000 TIME: 11:22:57

Input Set : A:\126pld1-s1.txt
Output Set: N:\CRF3\11062000\1348815.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]